

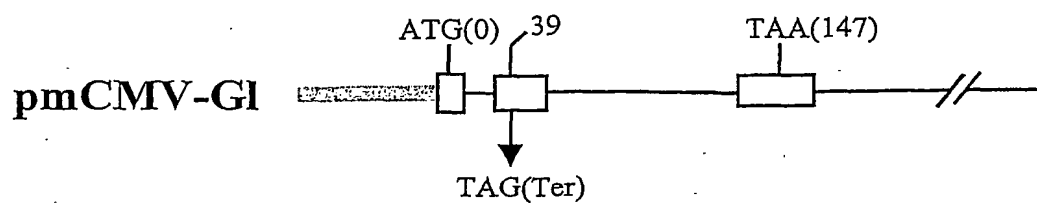
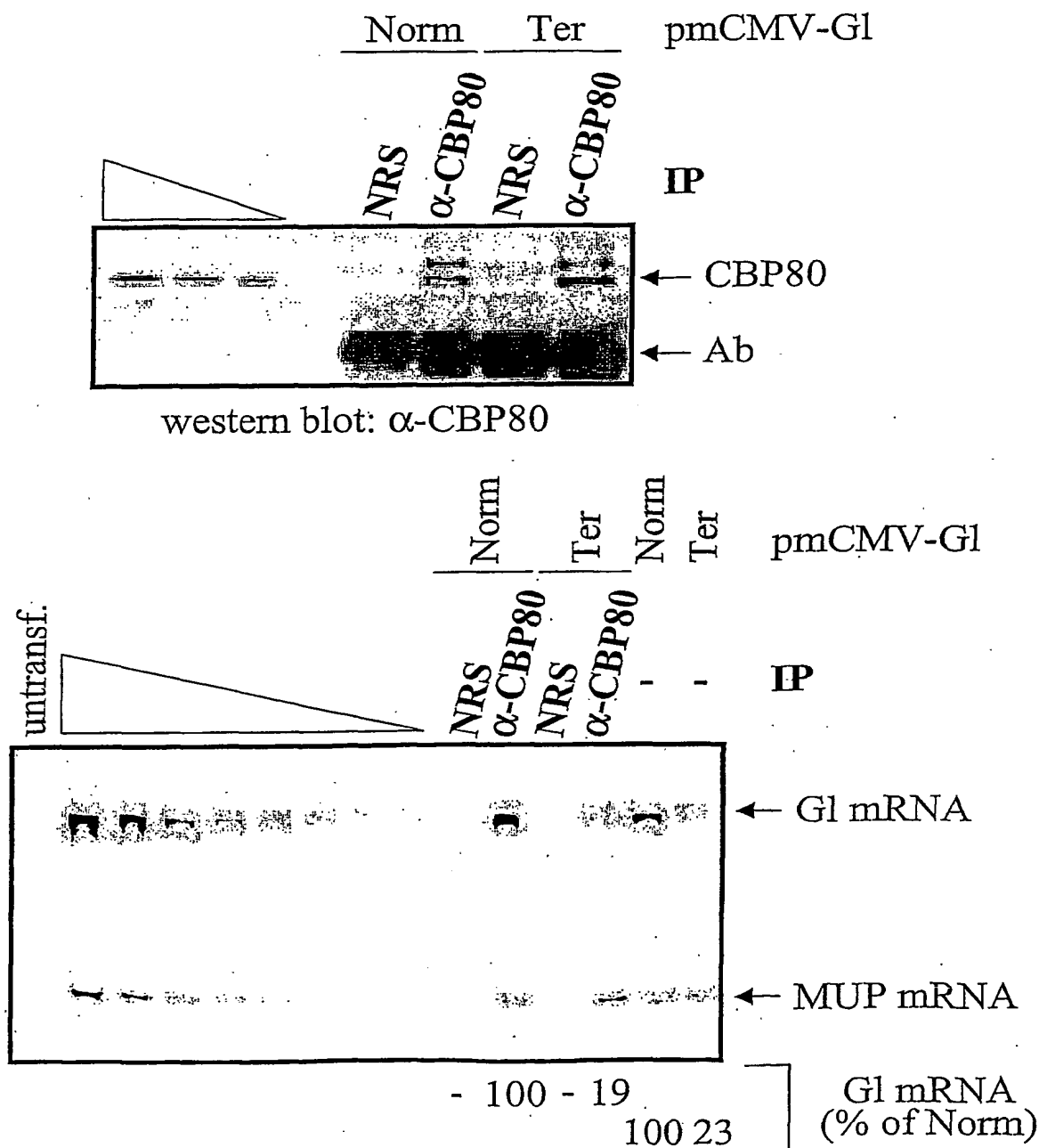
A**B**

FIG. 1 BEST AVAILABLE COPY

	Norm		Ter		Norm		Ter		pmCMV-Gl	% of cell protein in IP	
	NRS	α -CBP80	NRS	α -CBP80	NRS	α -eIF4E	NRS	α -eIF4E	IP	α -CBP80	α -eIF4E
8×10^5 cells									α -CBP80	34 \pm 2	0
									α -eIF4E	0	15 \pm 1
32×10^5 cells									α -CBP20	26 \pm 2	0
									α -eIF4G	2 \pm 1	10 \pm 4
									α -PABP2	11 \pm 1	0
									α -Upf 1	0	0
									α -Upf 2	9 \pm 3	0
									α -Upf 3	7 \pm 1	0
									α -rlpL10	2 \pm 1	14 \pm 3

Norm Ter Norm Ter Norm Ter
 α -CBP80 α -CBP80 α -eIF4E α -eIF4E
 NRS NRS NRS NRS - - IP

← Gl mRNA

← MUP mRNA

- 100 - 17

-100 - 12

100 20

Gl mRNA
(% of Norm)

FIG. 1

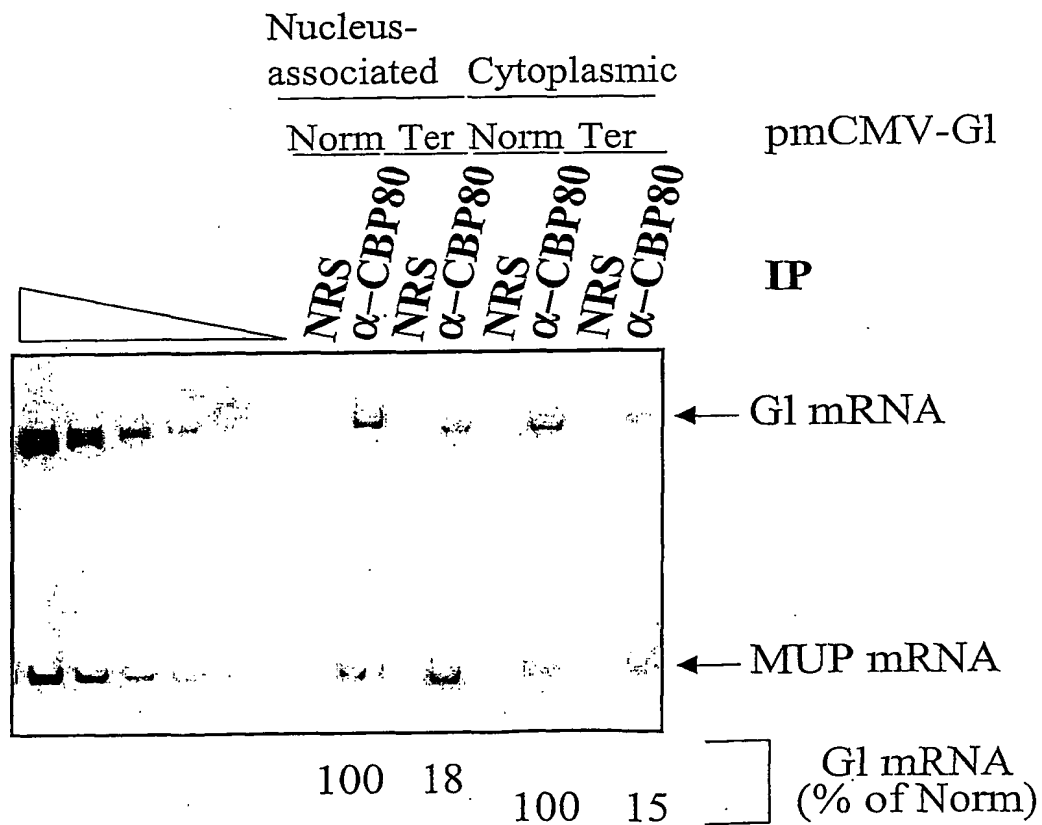
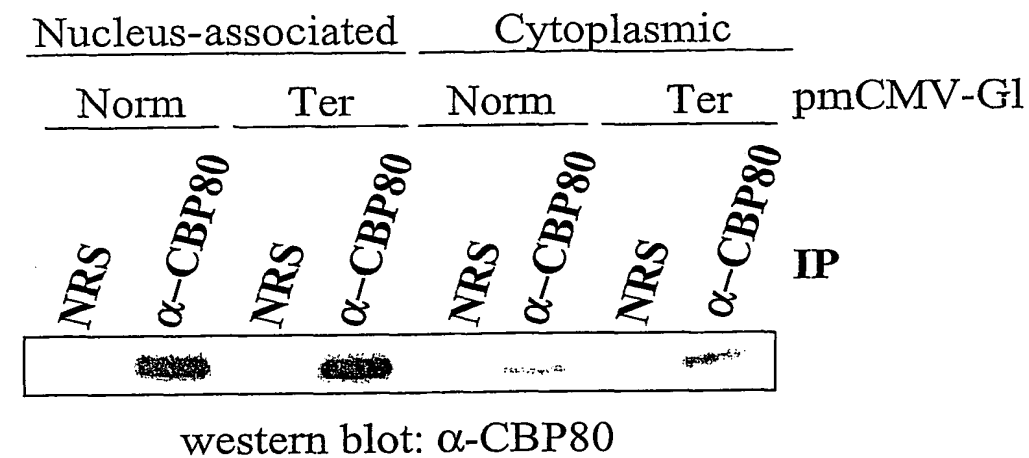


FIG. 2

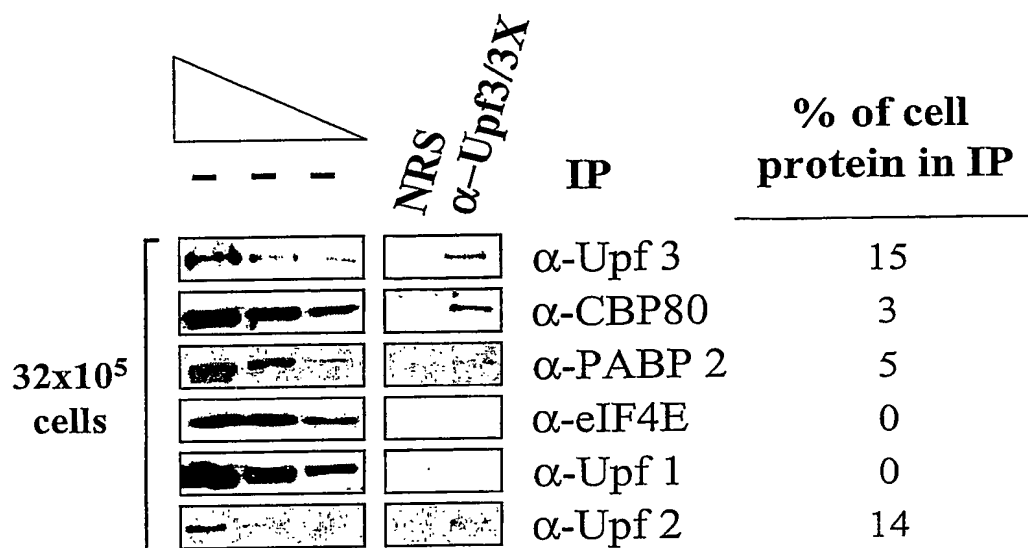
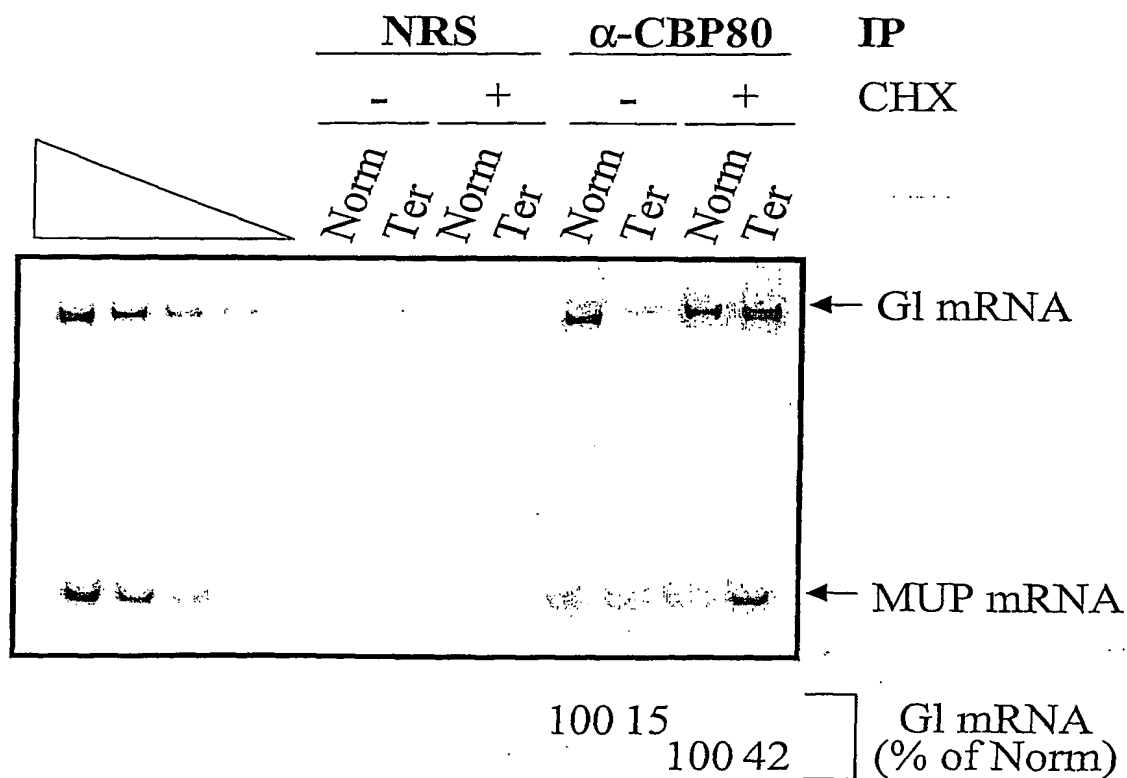
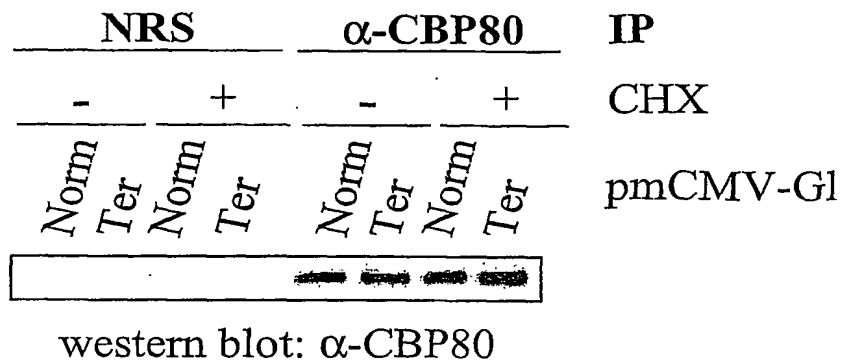


FIG. 3

A**FIG. 4**

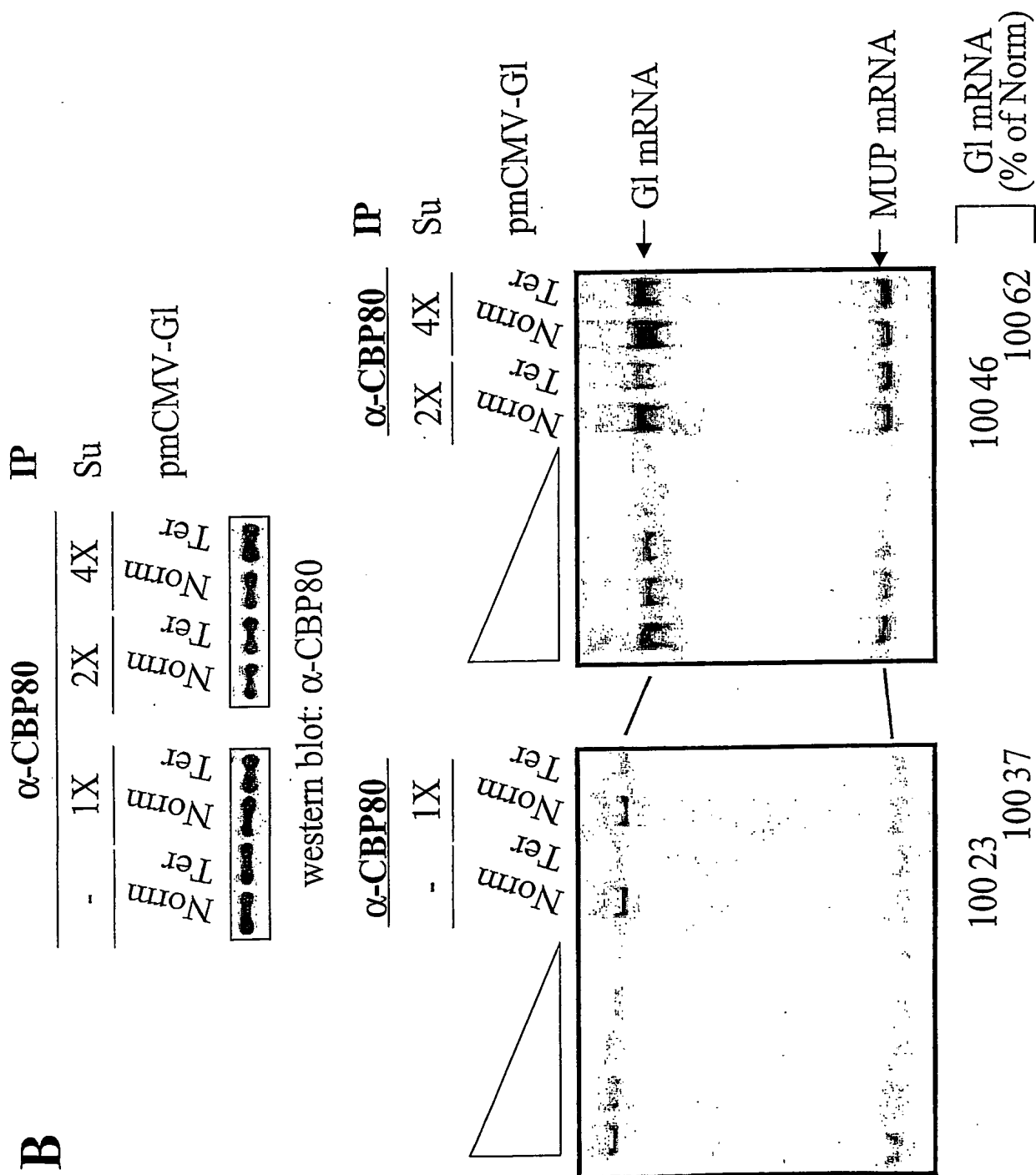


FIG. 4

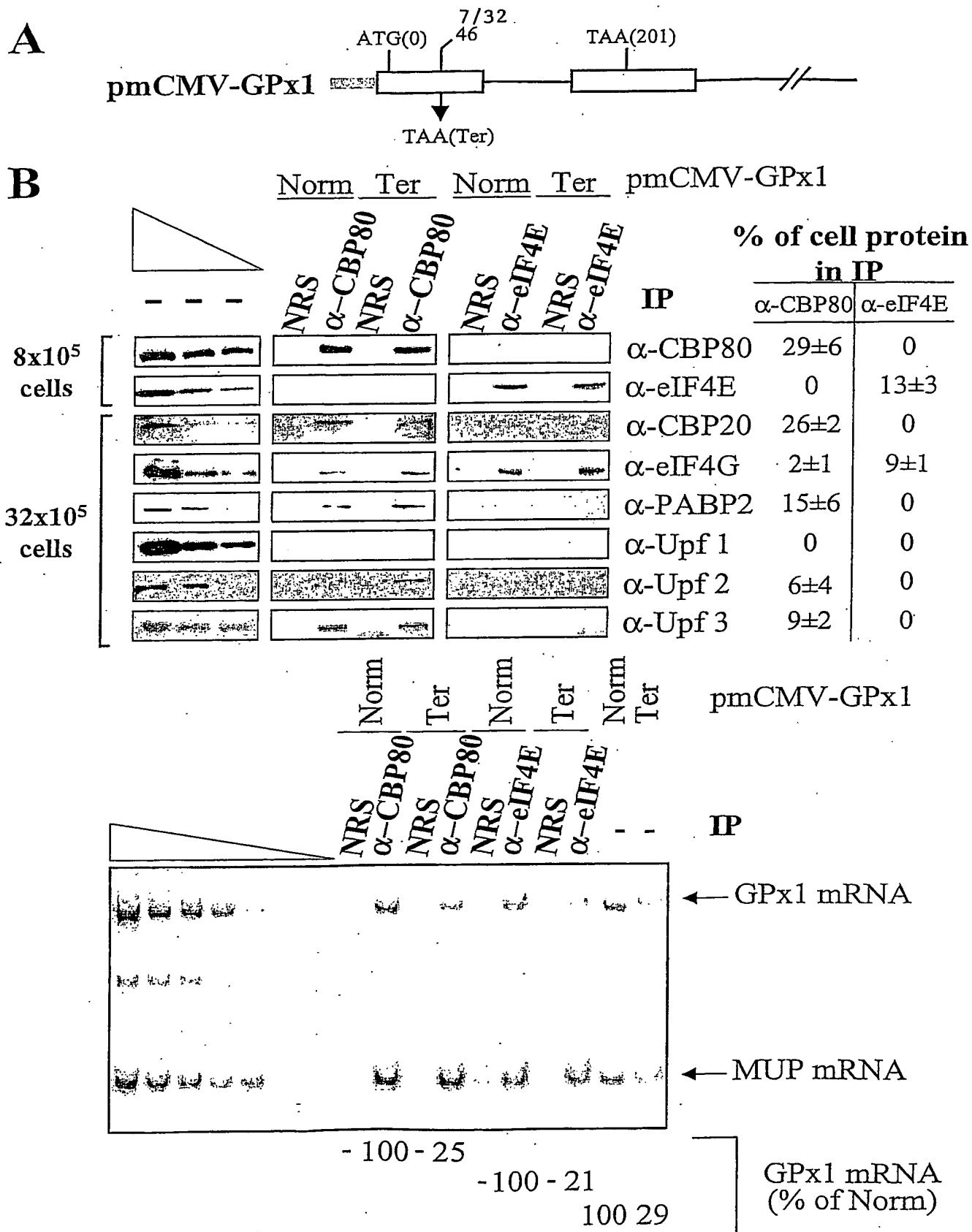
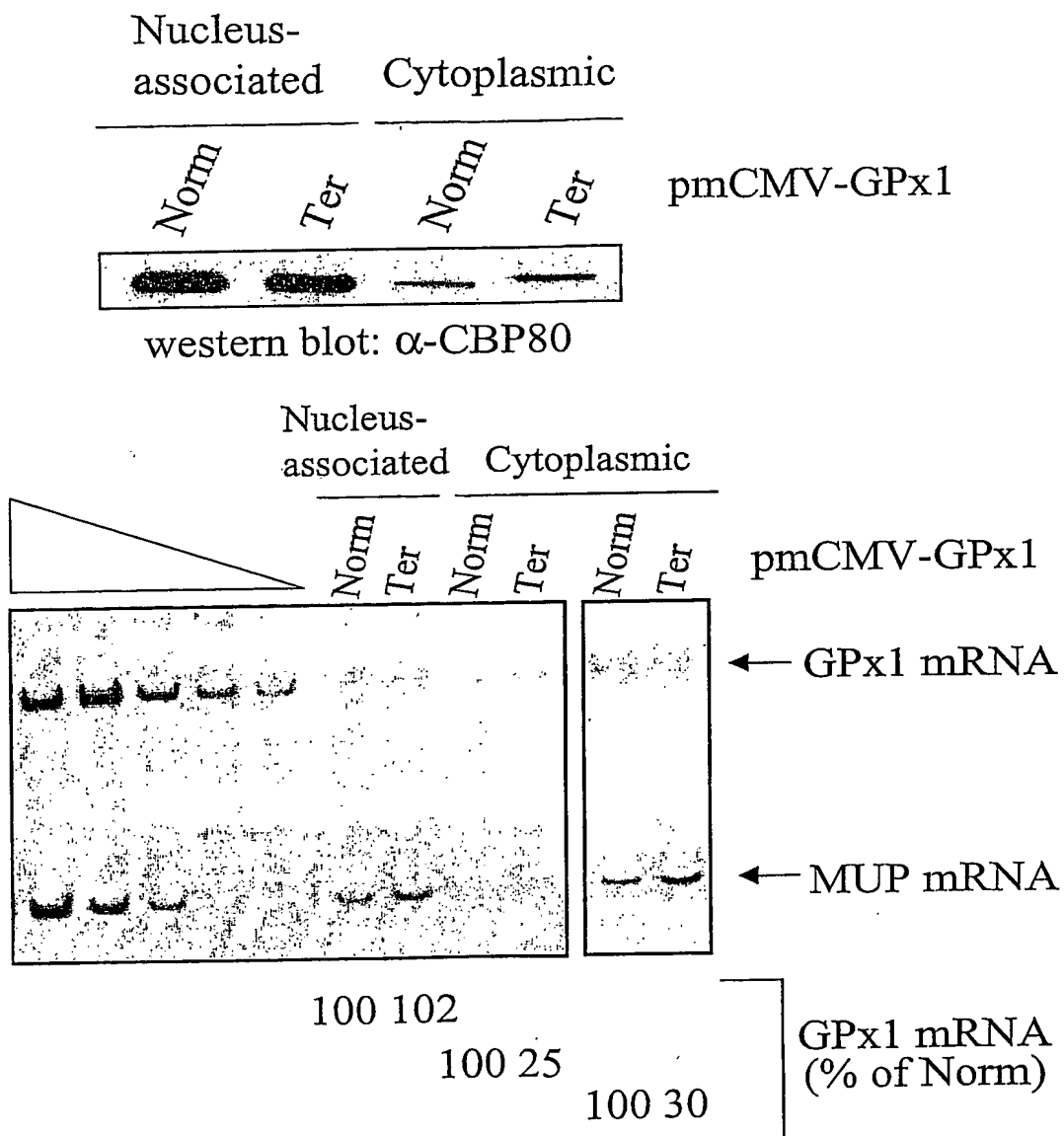


FIG. 5

**FIG. 6**

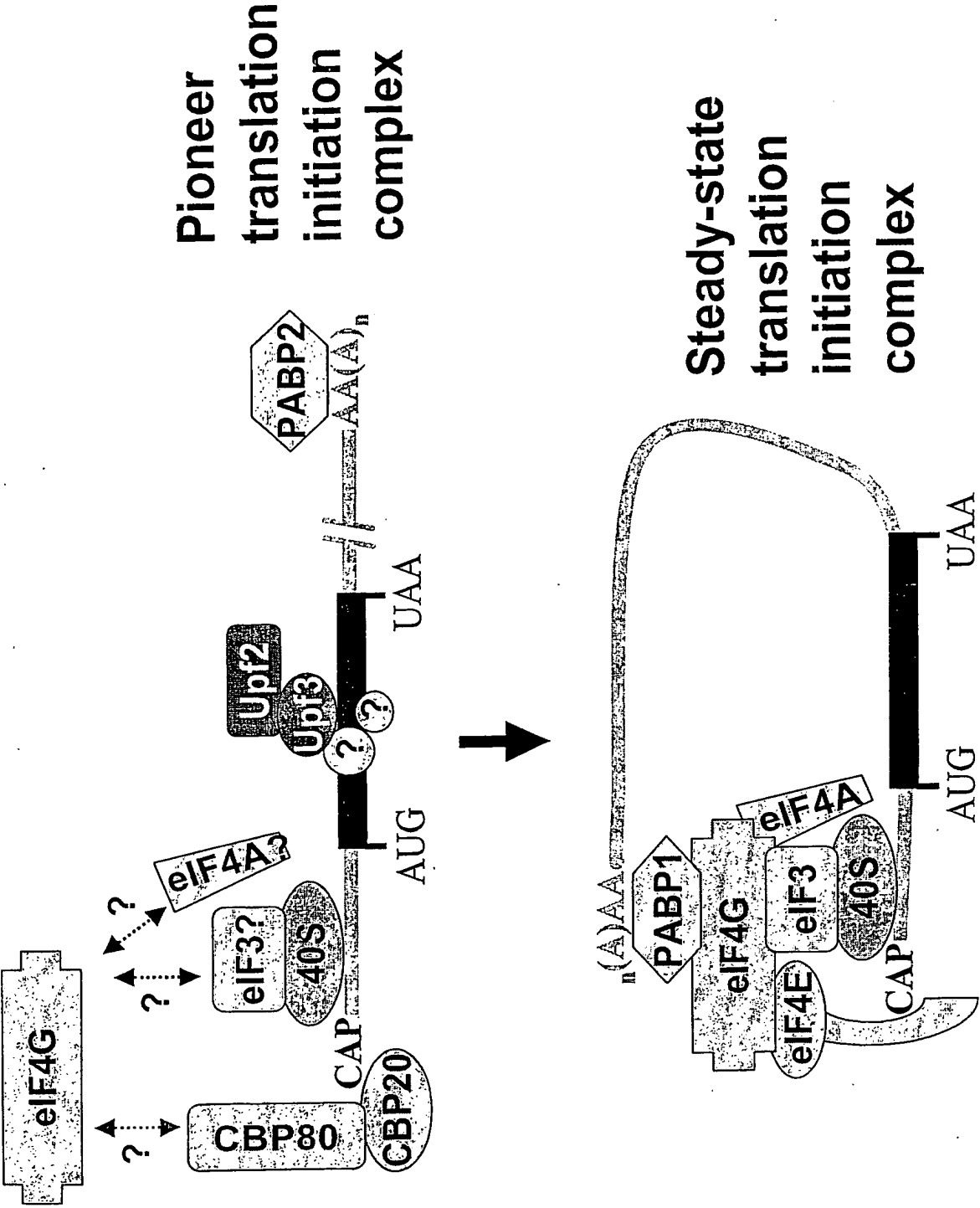


FIG. 7

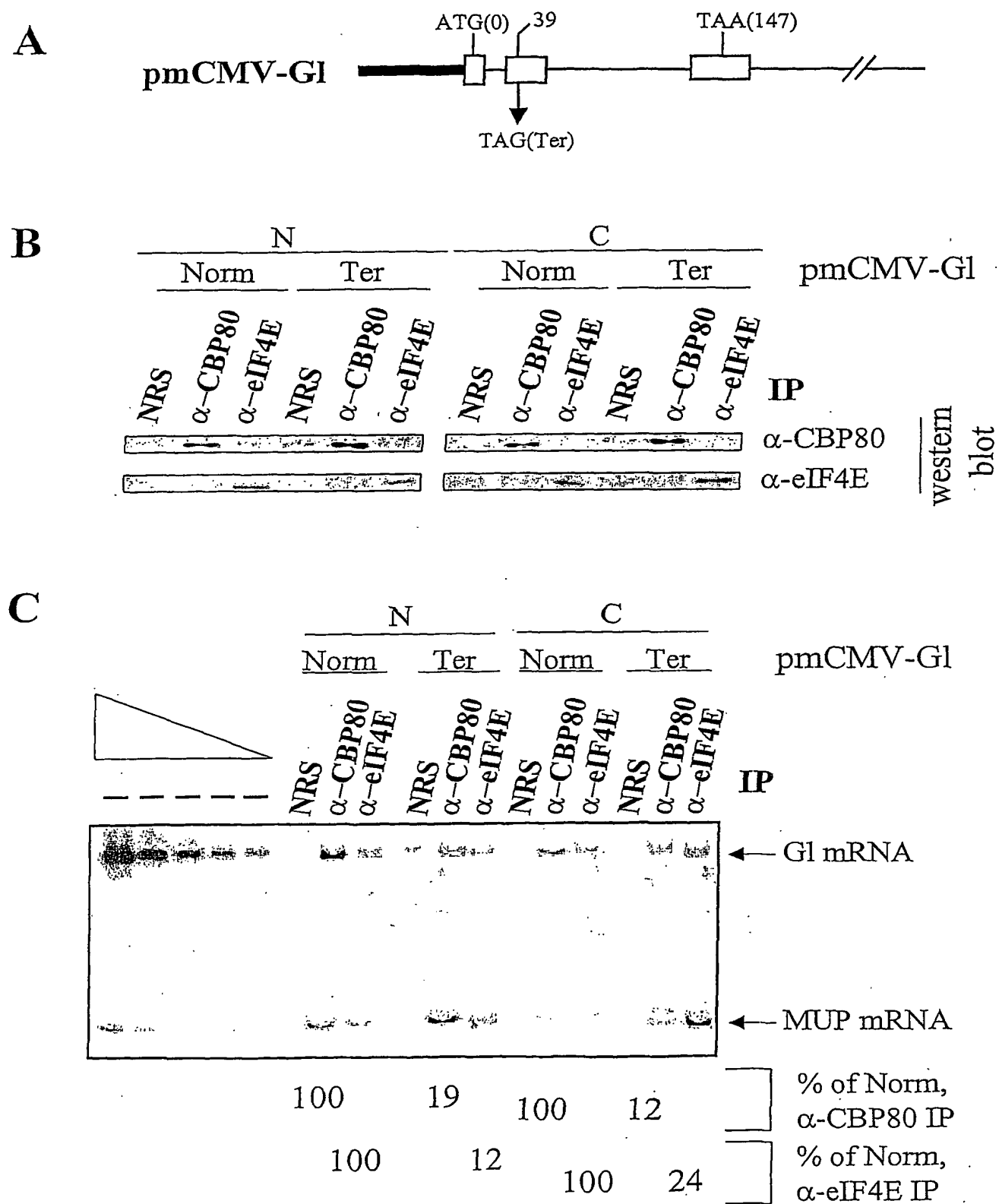
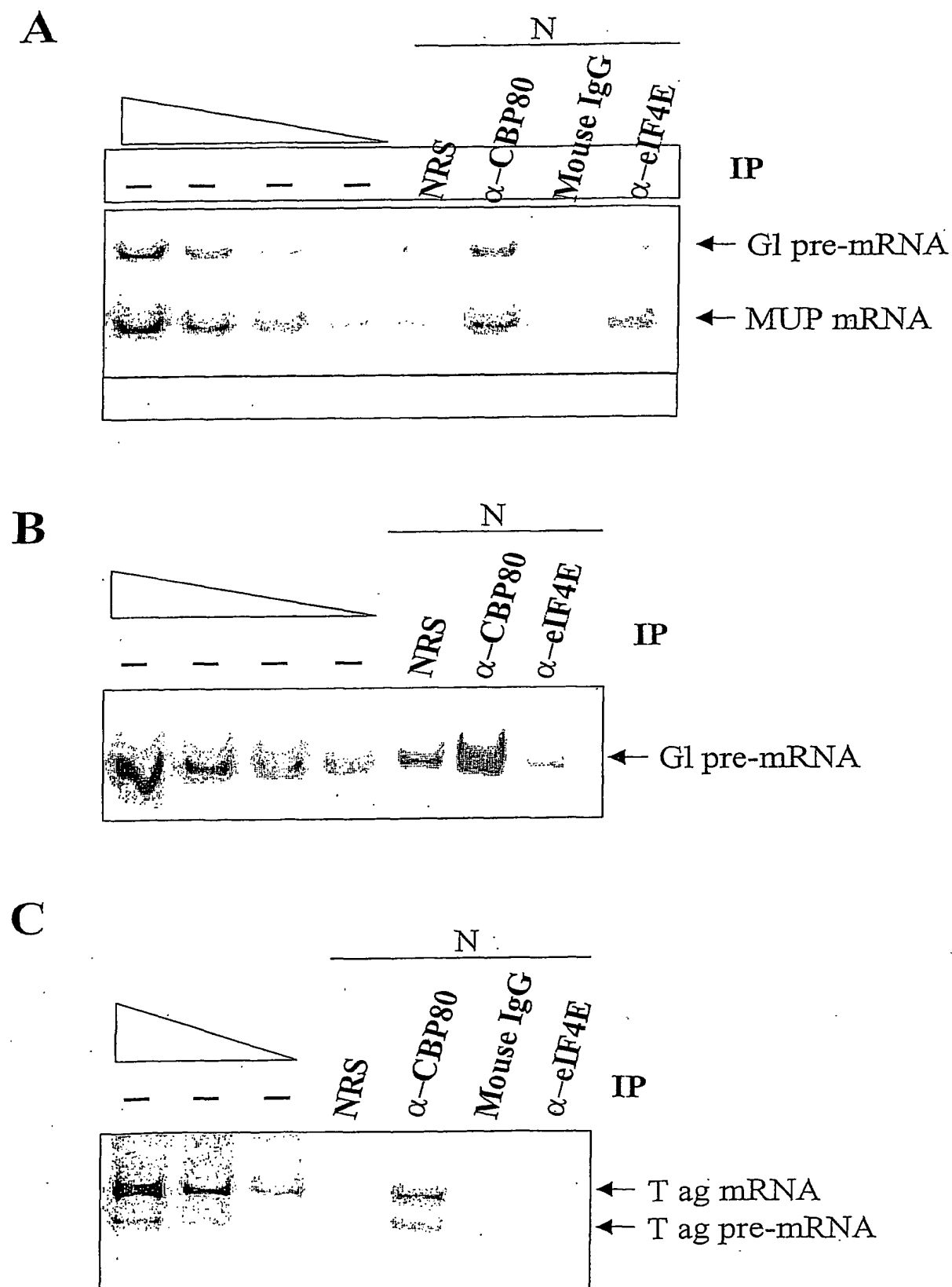
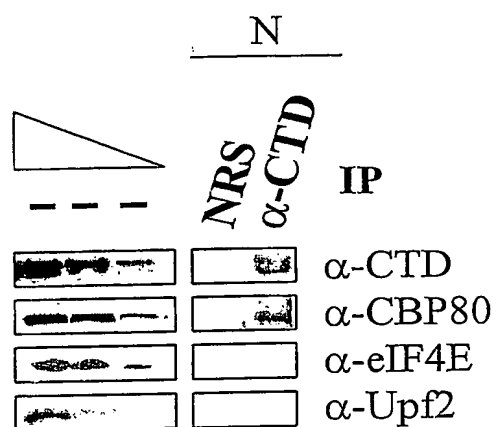


FIG. 8

**FIG. 9**

**FIG. 10**

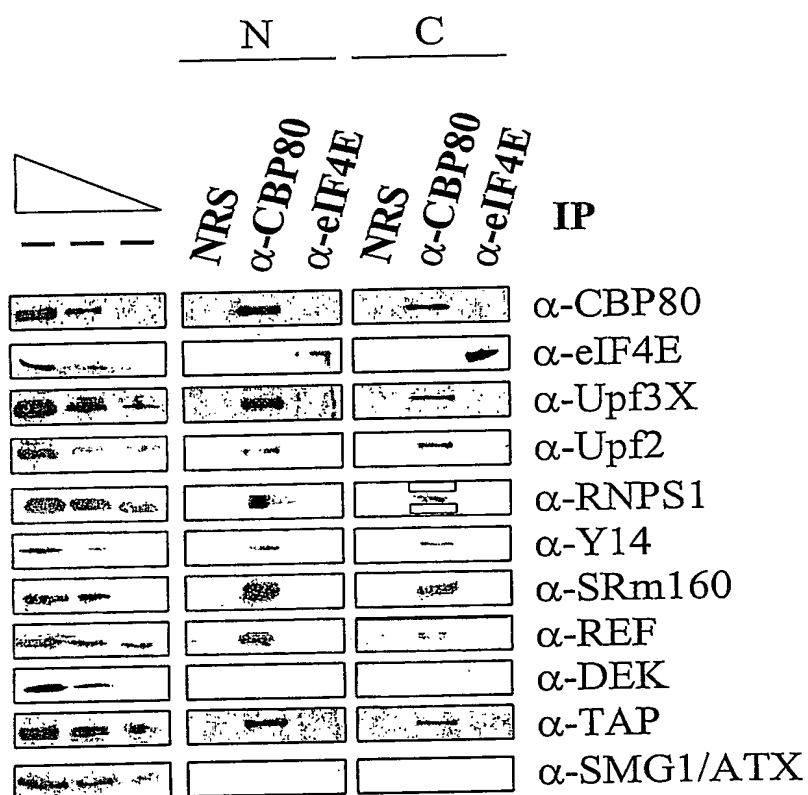


FIG. 11

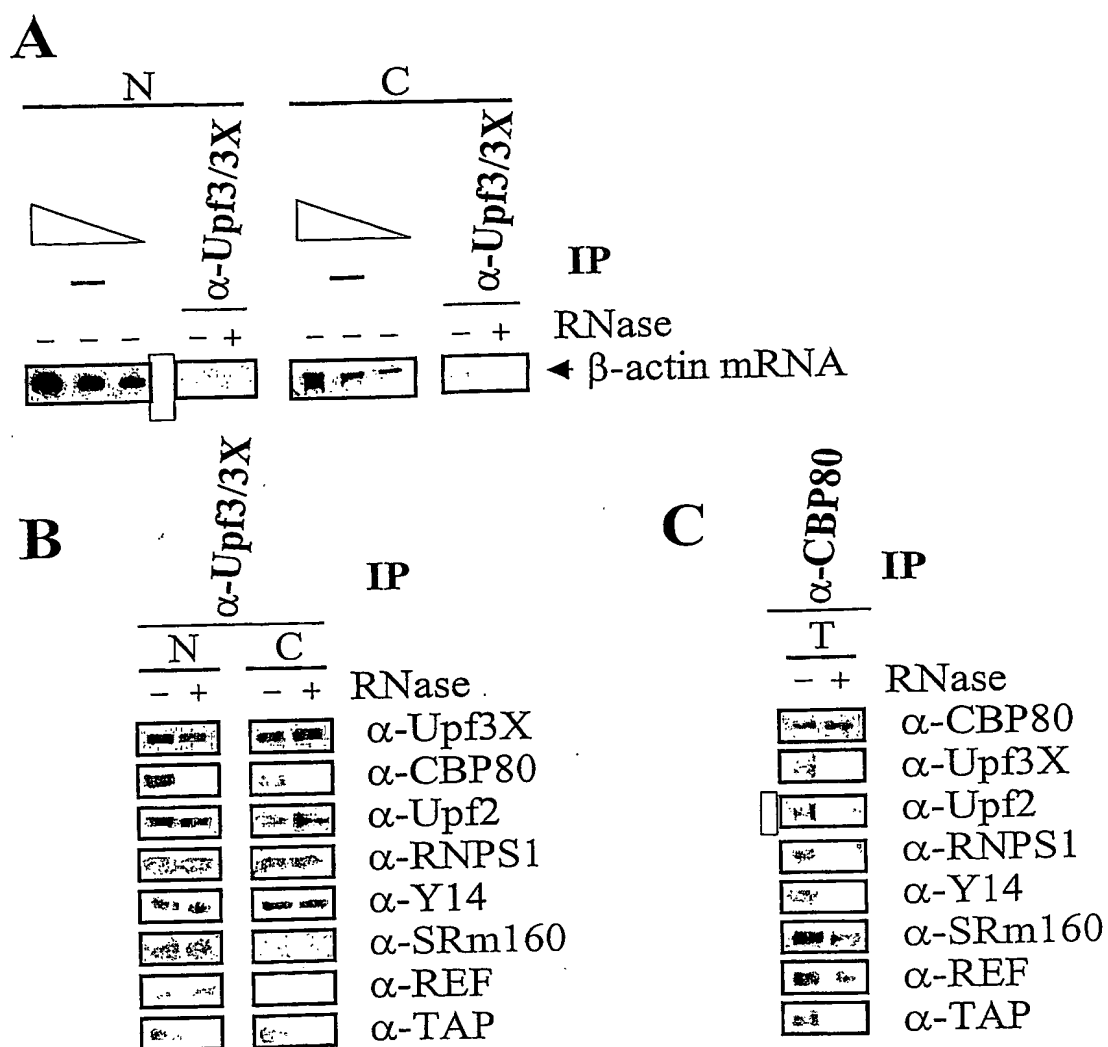


FIG. 12

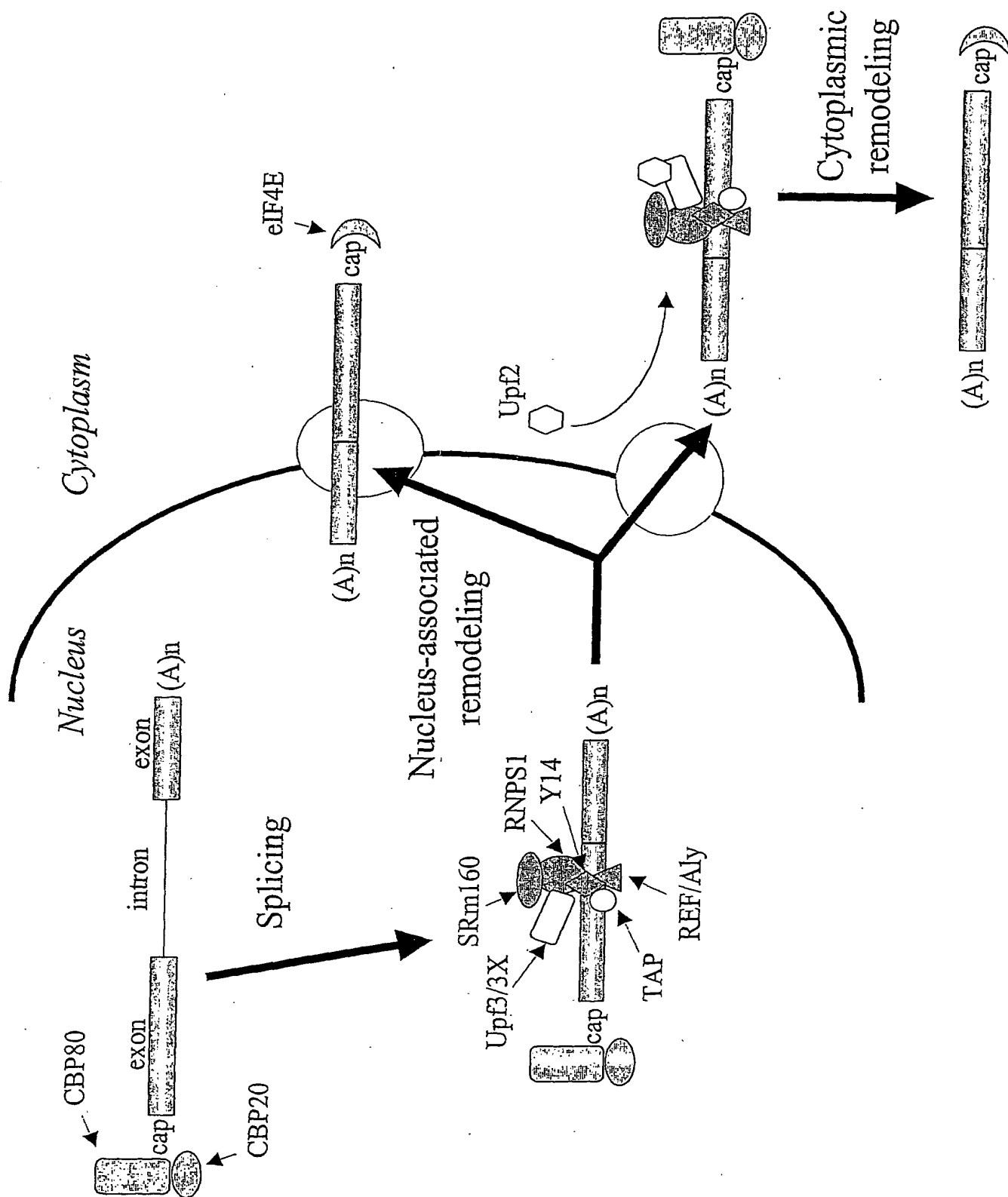


FIG. 13

A

MAEGLERVIRISASELRLGILATLAPQAGSRENMKELKEPRKONRRPDLEIYKPLSRLNPKIKKEPPGSEEPKDEIVN : 80
 DRDCSAVENGTQPVKDVCKELNNQEQNGPIDPENNRGQESFPRTAGQEDRSIKI KRTKKPDLQIYQPGRRLLQTVSKESA : 160
 SRVEEEVLNQVQLRVBEDECRGNVAKSEVANKPDRAEIEKSPGGGRVGAAGKEGKRMKGEGVRETHDDPARGRPGS : 240
 AKRYSRSDKRRNRRTSTSSAGSNNSEAGAGLTDNGQRRRQDRTKERPPKKQVSVSSSDSLDEDRIDEPDGLGPRRS : 320
 S[RKRI]ERNWSGRGEGEQKTSKEKYRGLRVTFDAEMNKESPMVRSARDDMDRGKPDKGLSSGGKSGSEKQSKNPKQE : 400
 LRGRGRGILILPAHTLSVNSAGSPESAPLGPRLFLFGSGSGKSRSHRGGTTTRLLWDPNNPDQKPAKTKTQPLHFLDTD : 480
 DEVSPTSWGSQQAQASYYKQNSDNPPYYPRTPGPASQYPTGYNPLQYVPGTNGVYGPYYPGYPTPSGGYVVCPLP : 560
 TSMTSPREEVQHMRNLQQQELHRLLRVADNQELQLNLLSRDRISPEGLEKMAQLRAELLQLYERCLLLDIEFSDNQNV : 640
 QILWKNAFYQVIEKFRQLVKDPNVENPEQIRNRLLELLDEGSDFFDSLLQKLVQVTKFLEDYMDGLAIRSKPLRKTVKY : 720
 ALISAQRCHMICQSDIARYREQASDTANYGKARSWYLKAQHIAPKNRFPYNQLALLAVYTRRKLDAVYYYYMRSLAASNPIL : 800
 TAKESLMSLFEEETKRKAQMEKKQHEEFDLSPDQWRKGGKSTFRHVGDITTRLEIWIHPSPRPSQGTESGKDSSENGEL : 880
 GSLSPSDDLNRFPILSFLHAHGKLFTRI GMETTPAVAEKVLKEFQVLLQHSPPSIGSTRMLQLMTINMFAVHNSQLKDCFS : 960
 EECRSVIEQAAALGLAMFSLVRRCTCLLKEZSAKAQLSSPEQDDQDDIKVSSFPVLDKELLPVSKVSDWMLGYPDTW : 1040
 NPPPTSLDLP SHVADVWSTLADF CNILTAVNQSEVLYKDPDDDLTLLLEEDRLLSGFVPLAAPQDPYVEKTSKDKV : 1120
 IAADCKRVTVLYFLEALCGEPEPLAFKGGKYVSVAFVPTDMGKEMSGEQGTREDEEEDVVIDFEEDSEAGSGGDED : 1200
 DIRELRAKIALAKAEQORRQEKIQAVIDESQMRQMELEIRPLFLVPTNGFIDHLASLARLLESRKYLIVVPLIVT : 1280
 NELDGLAKGQETDHRAGGYARVVOEKARKSIEFLEQRFSRDSCLRALTSRQNELESIAFRSEDITGOLGNNDLLILSC : 1360
 LHYCKDKAKDFMPASKEEPIRLLEVVLLTDDRNLRVKALTRNVPRVDIPAFITWAQVG : 1419

B

CCTGGCTGCGCCGCGCGTGGCGGAGCCGCTACGCGCTGTAGCAGCAGCCGGAAGCTGGCGGAGGCGTGGAGCGTGTGGGAGTCTCCGCGTGGAGCTG : 100
 CGCGGGATCTGGCTACTCTGGCCCGCAGGCGCGGAGCAGAGCAAAACATGAAGAAATTAAGAGAGGCGCGCGCAAGATAACAGGCGTCCAGATC : 200
 TGGAAATCTATAAGCTGGCCCTTCTCGCTAGGAACAGCCCAAAATCAAGAAACCCCTGGAGTGAAGAAATCAAGAGTGAATTTGTAATGACCG : 300
 AGGATGCTCTGCTGTGTAATGATGACACAGCCGCTTAAGAGATCTCTGCAAGGAACCTGAACACCAAGAGAGAGAGTGGCTATAGACCCCAAGAAATAT : 400
 CGGGGACAGAAATCTTCTAGGACTCTGGACAGAGGAGTGTAGTCTAAAGAAATATCAAAAGAACCAAGAAACCGAGCTCGACATCTATCAGACATG : 500
 GACGACCTTTGACAGCTGTAGCAAGAAATCCGCGAGTCCGCTGGAGGAGAGAGAGTCTCAACAGGAGTGAACCACTAGAGTGTAGAGAGAGATGAGT : 600
 TAGGGGAAATGTTCGAGGAGGAGAGTGTGGAATAAACACAGACAGGGCGAGATAGAAAGAGCCAGGCTGGGAGAGTAGGGGCTGCAAAAGAGAA : 700
 AAAGGAAAGAGAGTGTGGAAGGAG : 800
 AACGAGGAAATCGCTACGCAACGCGCAGCAGCAGCTGAGCAGCAACCAACGCTGAGGAGGAGTGGCTGAGCGATAATGATGTCCGCGCGGCG : 900
 ACAGGATAGGACCAAGAGAG : 1000
 GGACCCAGGAGAGTGTGAGAAAGGAGAGACATTTAGAAAGAACTGGTCTGGCGCTGGGAGGAGTGAAGCAGAAACCAAGTGTCAAGAAATATCAGAGCA : 1100
 TCTCTCTGTCTACTTTCGATGAGAG : 1200
 GAGCAGGAG : 1300
 ACCCTATCTGTCTCAATTCAGCAGGTTCTCGAGAGTCCGCGCTTTGGGAGCTCGGCTTTTGTGTGATCTGGTAGTAGGAGTCTCGGAGTGTGGGCG : 1400
 GAGGACCAACACGCGGATTTGGGAGCCCAACCAATCTGATCAGAAACCTGCTCAAGACTCAGACGCCCCAGCTACATTTCTTGACATCTGATGATGA : 1500
 AOTCAGCCCTACATCTTGGGAGTCTACGCGCAGGCTCAGGCTCTTACTAAGTTTCAAACTCTGACCAACCCCTATTATTACCCCGGAGCAGCAGG : 1600
 CCGCTCTCCAGTATCTCTATACGGGCTATACCCCTCTACAGTACCCAGTGGGCGCTACGAATGGTGTGTAACGAGGCGCTTACTACCCAGGCTACCCGA : 1700
 CTCTGTCAGGACGATATCTGTGTAGCCCTCTACTACAGCAGCAGTGTAGTCCCGAGGAGGAGTGAAGCAGACATGAGGAGCCTGACAGAACAGGAGCTGCA : 1800
 CAGGCTCTCTCGGCTGGCTGACCAACAGGAACTGACAGCTCAGCAACCTGCTCTCGAGGACCGCATCAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAG : 1900
 ATGAGTGAAGTGTGCTGAGCTATATGAGGCTGTATCTATTAATGATGAGTCTCTGATAATCAAGATGTGATGATGATGATGATGATGATGATGATGAT : 2000
 ATCAGGTGATGAG : 2100
 TGACTTCTTGTATGAT : 2200
 ARGACATGAAGTGTGCTGAGCTATATGAGGCTGTATCTATTAATGATGAGTCTCTGATAATCAAGATGTGATGATGATGATGATGATGATGATGATGAT : 2300
 GGAAGAGCAGCAGTGTGAT : 2400
 GCTTGAAGCTGTCTTACTATATGAGGCTGTATCTGAGCAGCAGGCTGTATCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG : 2500
 AAGCAGGAG : 2600
 ACACCTCTGCTGTGAT : 2700
 CCGAGTCTGCTGTGAT : 2800
 GCTGAGAG : 2900
 CAGTACACAGCTCCGAGCTGAG : 3000
 GGTCCGCGCTGTGAT : 3100
 GTCCGAGCTGAG : 3200
 TGCCCTGCGTGTGAT : 3300
 GGAT : 3400
 ACCTCGGAT : 3500
 AGGGTGGAGAGTATGAT : 3600
 GGTGATGAGAGTATGAT : 3700
 ATAGCTGAGCAGGAG : 3800
 TACAGACACCAAGCGCTTCAATGACCACTGGCCATCTGGCGCGCTGCTGAGAGCAGAGATACATCTGGTGTGCGCTCATCGATGATCAATGA : 3900
 GCTGGAGCGGCTGGCCAGGAG : 4000
 CAGCGATTCAGAGTGTGGGCTTTCGCTGGAGGCTGACGAGCGGTGCAATCGAATCCATCGCTTCCGAGTGAAGACATCACTGGCCAGG : 4100
 TGGTAAACAGATGATCTACTCTGCT : 4200
 ACTGCGGAGGAGTGTGCT : 4300
 GCGCAGGAGGAGTGTGCT : 4400
 TGCTGAGCCACCACTGCT : 4500
 GATCGGCGGAGGAGTGTGCT : 4600
 ATGCTCTCAGGCTTCTGCT : 4700
 GGTCTCAGAGTTCGCT : 4800
 AAGTGTGAGGAGTGTGCT : 4900
 CCCCACCTCTTACCT : 5000
 GGTCCGCT : 5100
 TCTTCTTCTGCT : 5200
 ACCCTCTTCTGCT : 5300
 TCTCTACTACCT : 5400
 GCTTGGAGGAGTGTGCT : 5500
 TGCCCTTCTGCT : 5600
 TTTGCTGAG : 5700
 CTGCT : 5800
 AAGACTGGGCTCTTGGAGTACAGGCTCCGCGCTCTCTTAAAGATCTCTTAAAGATCTCTTAAAGATCTCTTAAAGATCTCTTAAAGATCTCTTAAAGAT : 5900
 TCTCTCTCTGCT : 5965

FIG. 14

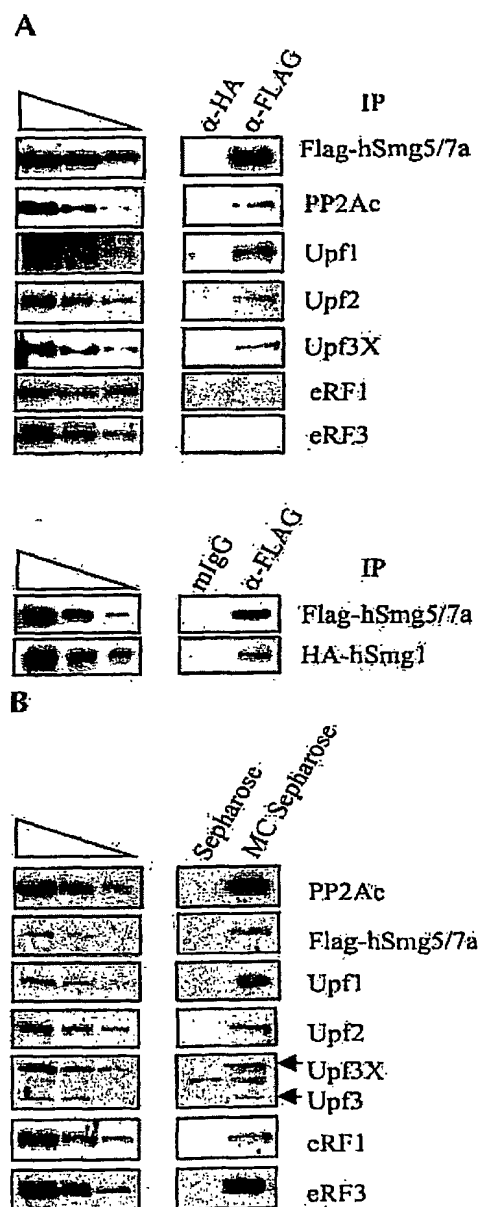


FIG. 16

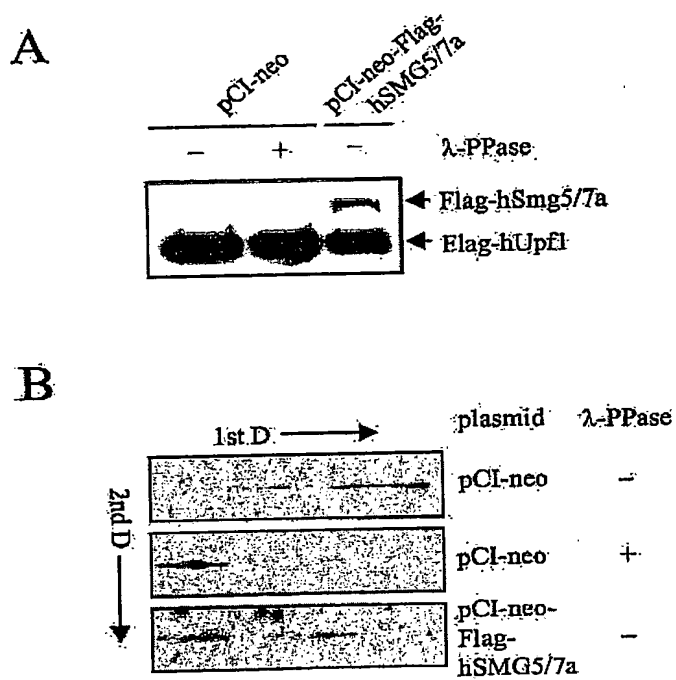


FIG. 17

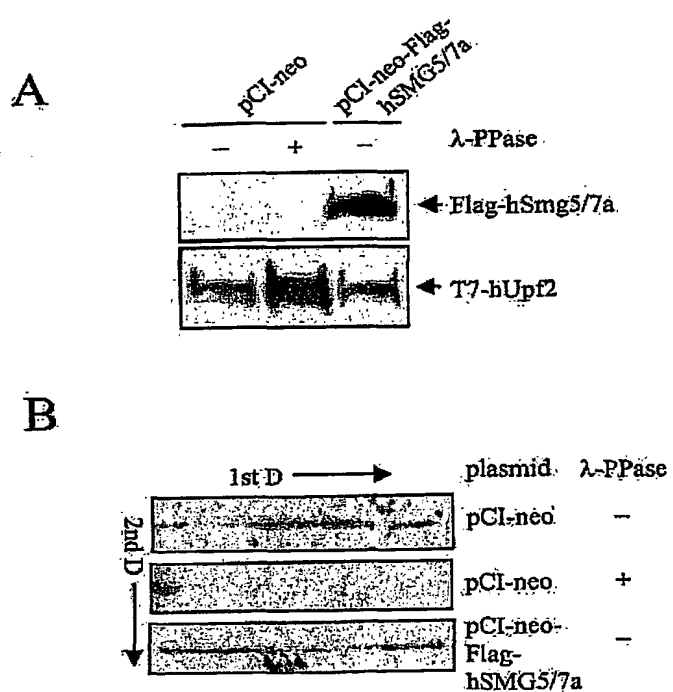


FIG. 18

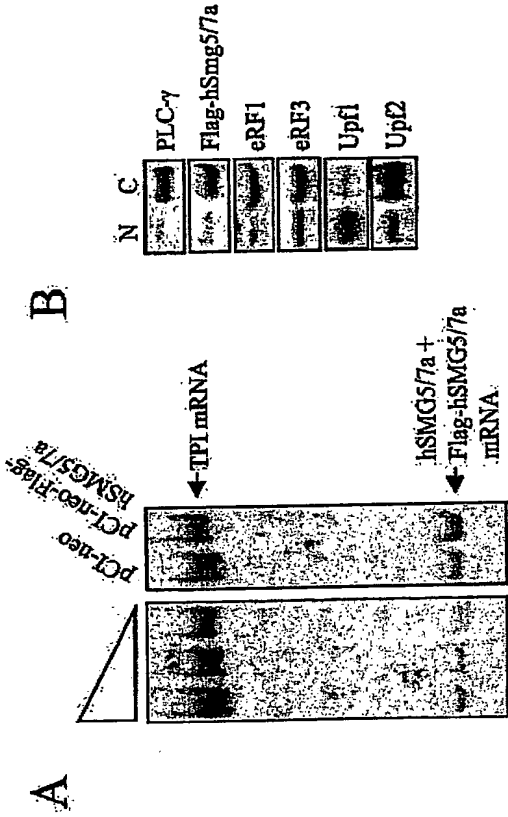
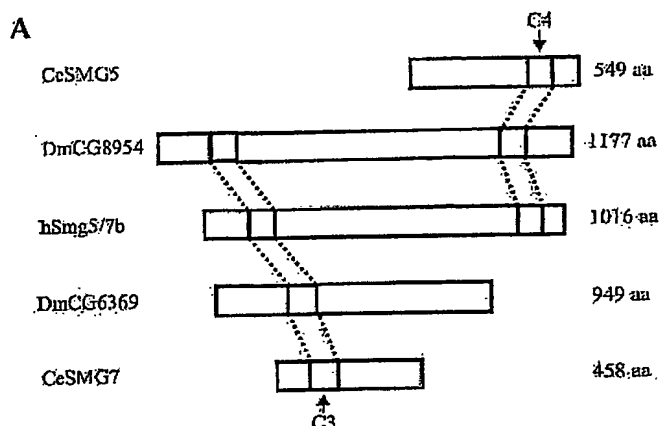


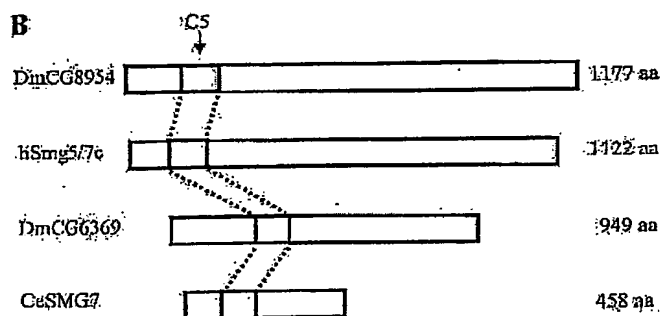
FIG. 19



C3

[illegible]

C4

[illegible]

C5

```

hsng577d :  VYBGPDAFY-----XNDS-SSVYRHAF-VPSNGVQI
CsSU7 :  GLRGDPLFY-----RHYVRYOYVSGCPNPS-VHIGU
DmCG6369 :  LGLGDLTFY-----VYKHVKAIFMVFYVQVPS-VF
DmCG8954 :  GLSGDPLFYELDPVNGKATISKEVYVYLVYVFEKDAEADQVCT

```

```

hsmg5/7c :  LASHKGDHETGCEGCGEAVETFGAAYTH
CEUMG7    :  LSH-LGAEHGBYQHTGAEHATMEPTSGGG
DmCG5369  :  LSYSHNRGDAVYQD-----TGKSE
DmCG8954  :  LHYGQTHNLETTHKSYKVCIGDEISEMNL

```

C

C3

Identity/ Similarity	hSmg5/7b	CeSMG7	DmCG8954	DmCG6369
hSmg5/7b		28%/54%	35%/59%	31%/54%
CeSMG7			28%/50%	29%/59%
DmCG8954				28%/50%
DmCG6369				

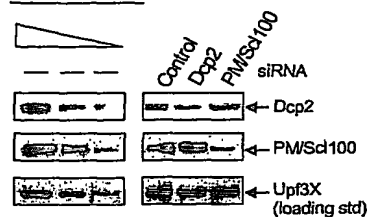
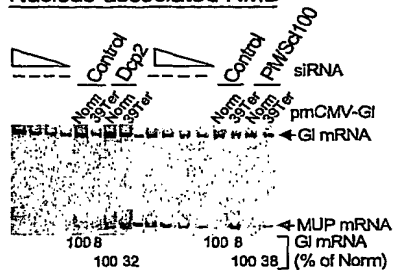
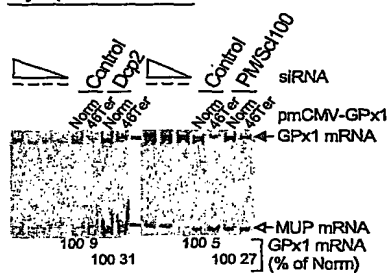
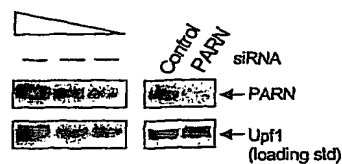
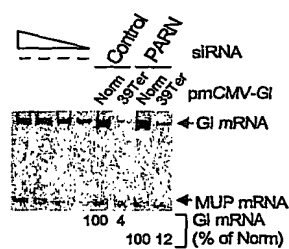
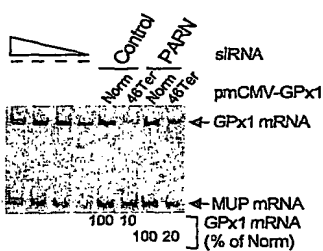
C4

Identity/ Similarity	hSmg5/7b	CeSMG5	DmCG8954
hSmg5/7b		27%/46%	37%/62%
CeSMG5			31%/51%
DmCG8954			

C5

Identity/ Similarity	hSmg5/7c	CeSMG7	DmCG6369	DmCG8954
hSmg5/7c`		27%/57%	35%/52%	30%/43%
CeSMG7			30%/53%	28%/46%
DmCG6369				30%/56%
DmCG8954				

FIG. 20

A. Down-regulation of Dcp2 or PM/Scd100Western blotNucleus-associated NMDCytoplasmic NMD**B. Down-regulation of PARN**Western blotNucleus-associated NMDCytoplasmic NMD**FIG. 21**

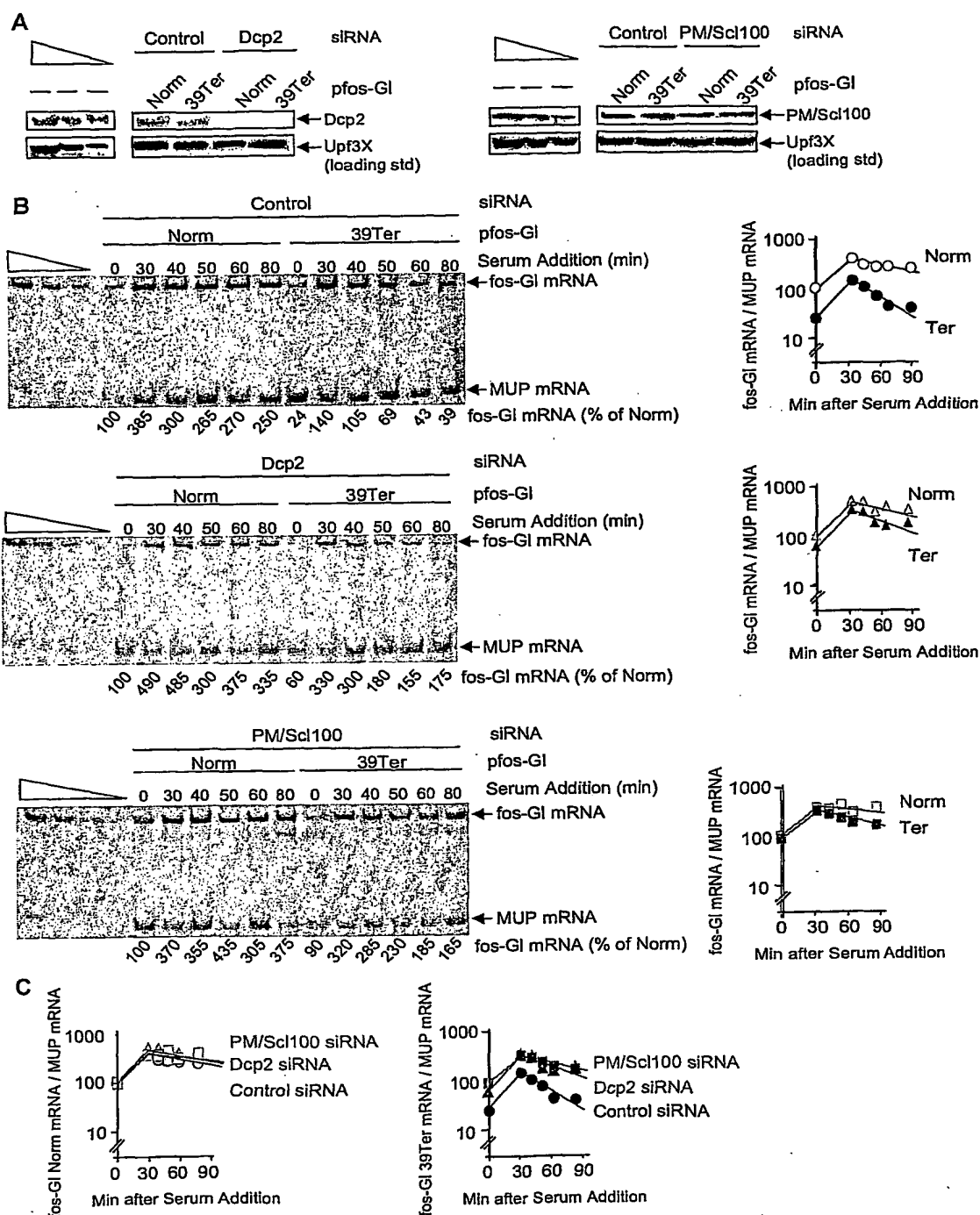
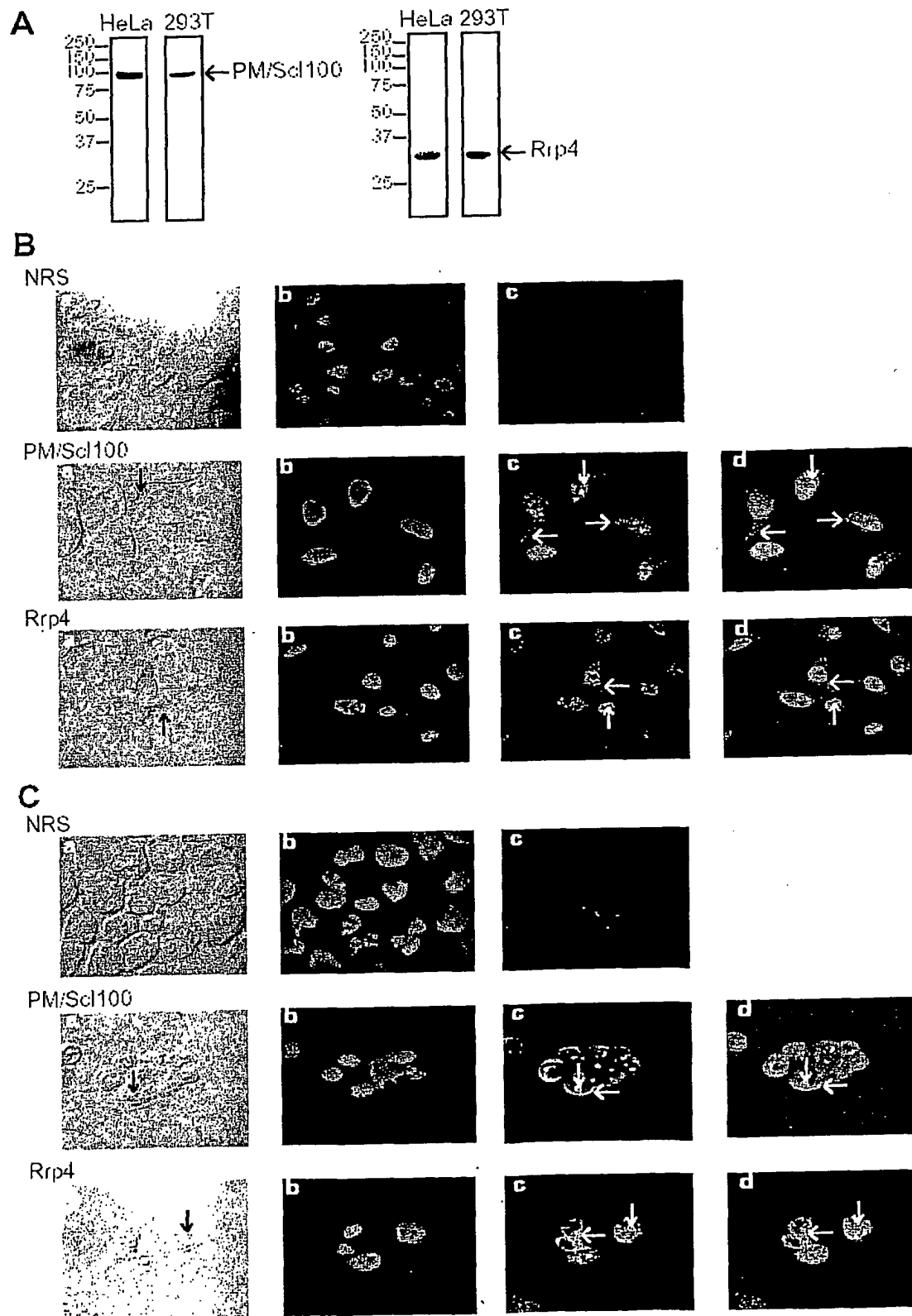


FIG. 22



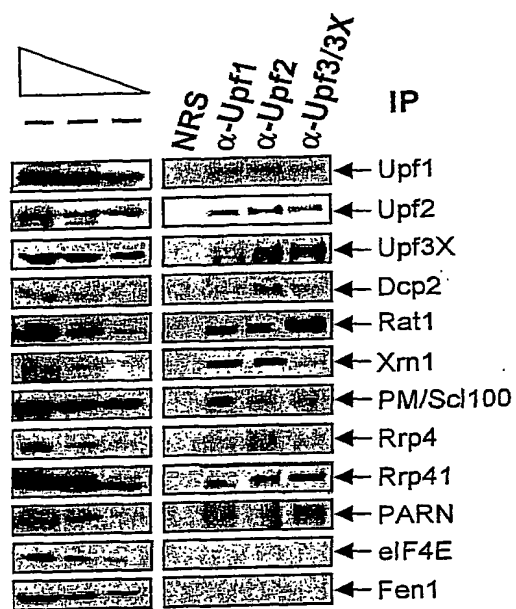


FIG. 24

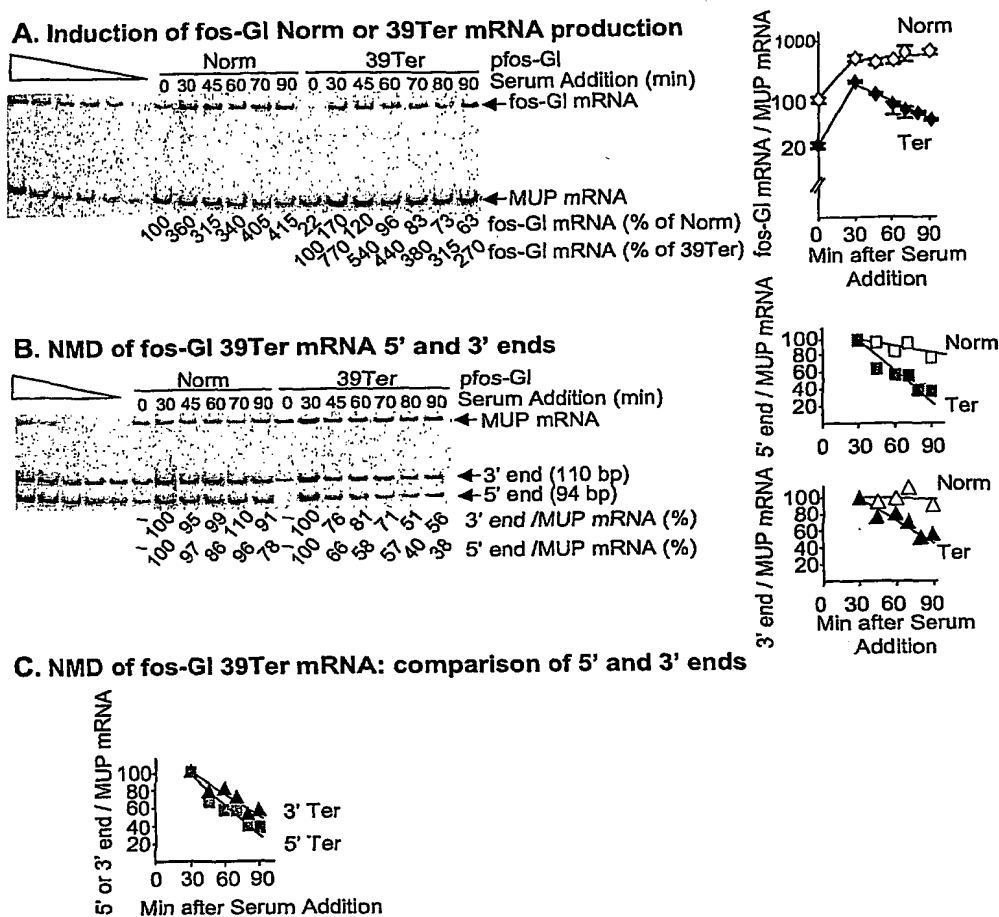


FIG. 25

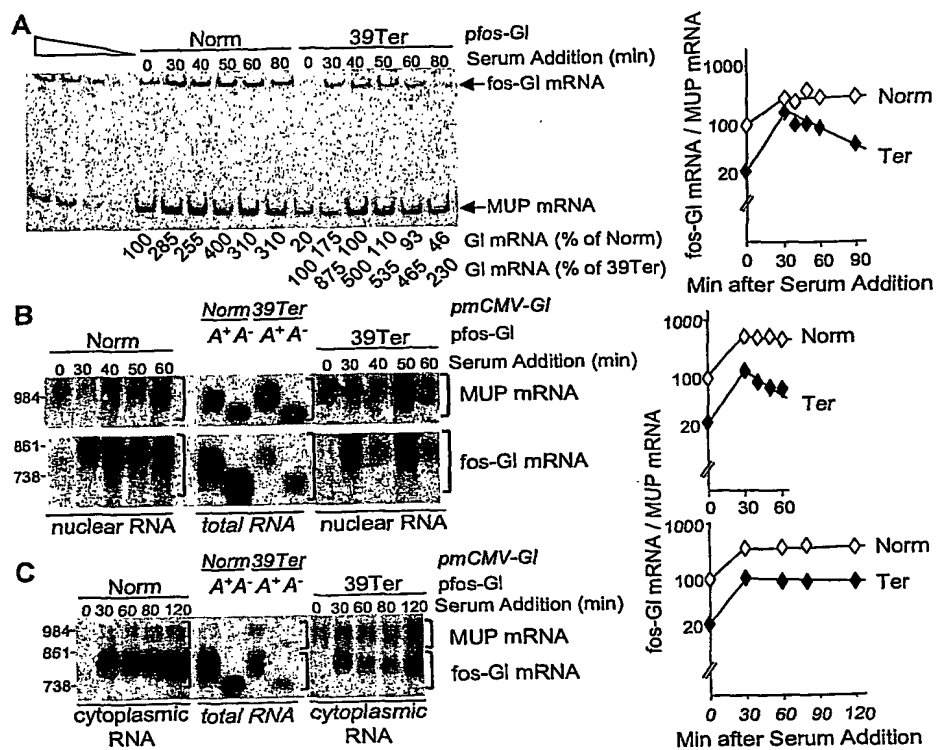


FIG. 26

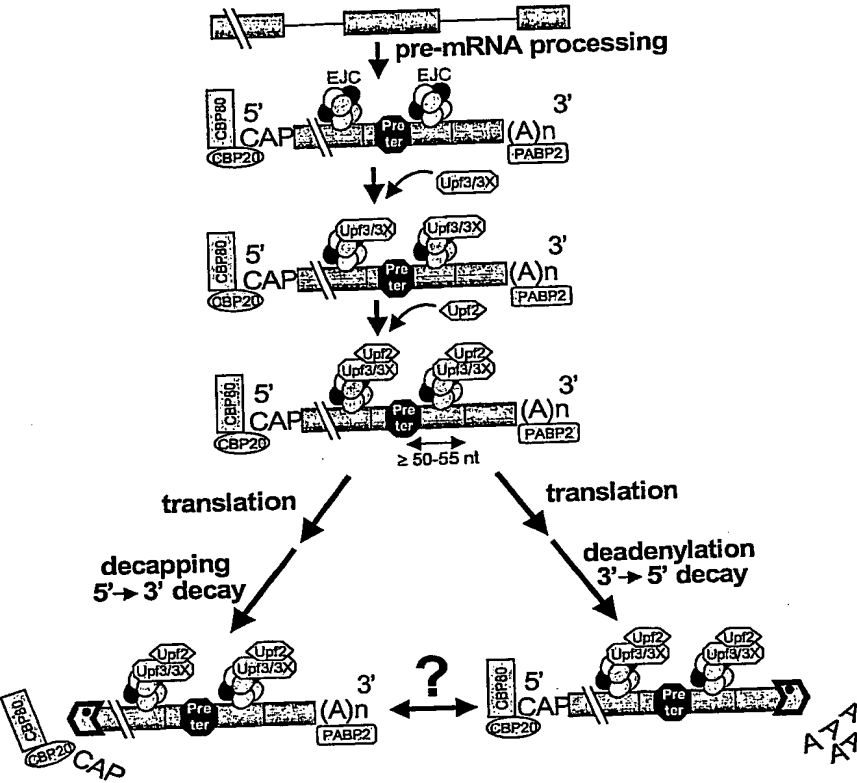
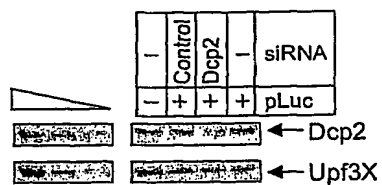
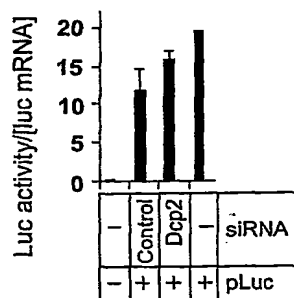
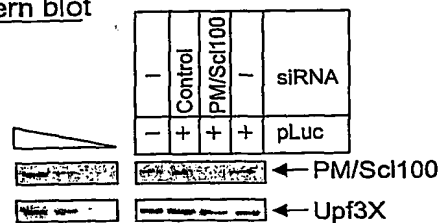
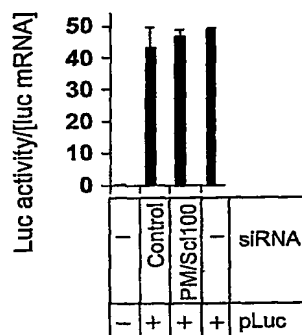
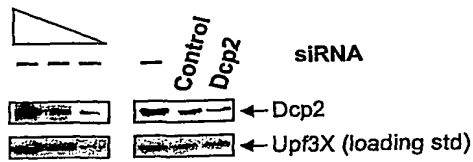
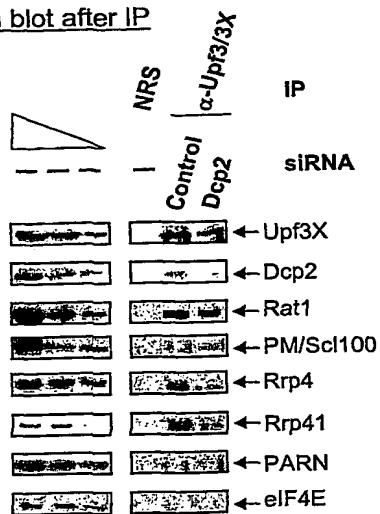
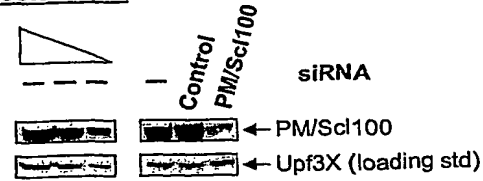
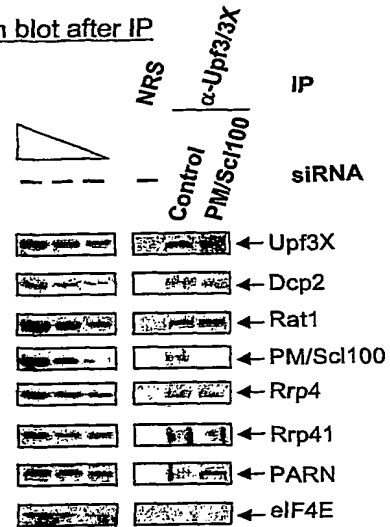
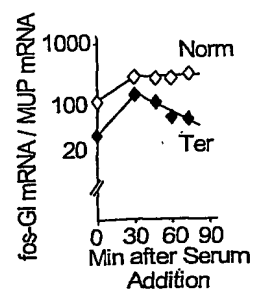
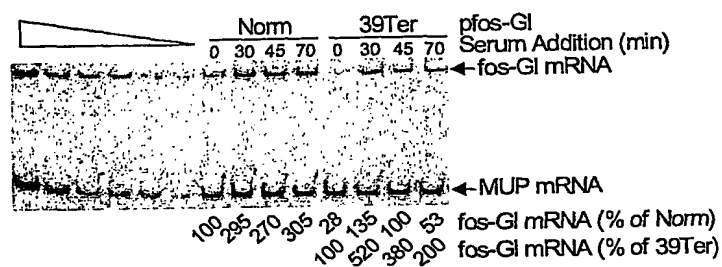
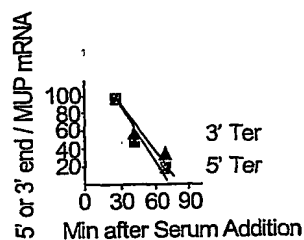


FIG. 27

A. Down-regulation of Dcp2Western blotLuciferase assay**B. Down-regulation of PM/Sci100**Western blotLuciferase assay**FIG. 28**

A. Down-regulation of Dcp2Western blotWestern blot after IP**B. Down-regulation of PM/Scf100**Western blotWestern blot after IP**FIG. 29**

A. Serum induction of pfos-Gl mRNA**B. Comparison of fos-Gl 39Ter mRNA 5' and 3' ends**

time end	30'	45'	70'
3' Ter	100	61	38
5' Ter	100	52	23

FIG. 30

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